

**Amendments to the Specification**

Please replace paragraph 268 (page 63 of the PCT publication) with the following amended paragraph:

[0268] The ORF of bnKCP1 gene codes for a 215 amino acid polypeptide product of polypeptide with several functional motifs (FIG. 11). Based on a search of protein localization sites using PSORT program (see URL:<http://psort.nibb.ac.jp>; Nakai and Kanehisa, 1992), bnKCP1 appears to be is a nuclear protein containing a pat7 nuclear localization signal (NLS) PLNKKRR (SEQ ID NO: 62; FIG. 10A, residues 127-133). Three acidic motifs (I, II and III) aid a serine-rich (S-rich) region (residues 34-58) may function in transcription activation by bnKCP1 (Johnson et al., 1993). The charged motif GKSKS (residues 88-143), which is conserved in all four protein orthologs (FIG. 10A), is rich in basic residues and encompasses the NLS. This suggests that this domain serve the may function of a DNA-binding motif (FIG. 11). In addition, bnKCP1 is extremely hydrophilic (FIG. 11) suggesting bnKCP1 is an active element in the nuclear matrix.

Please replace paragraph 294 (page 73 of the PCT publication) with the following amended paragraph:

[0294] BnIAA1 and BnIAA12 are clones ML2798 and ML4744, which are homologs of Arabidopsis IAA1 and IAA12, respectively, and were identified in a database of Brassica napus ESTs that were generated at the Saskatoon Research Centre of Agriculture and Agri-Food Canada (see URL:[www.brassica.ca](http://www.brassica.ca)).

Please replace paragraph 303 (page 75 of the PCT publication) with the following amended paragraph:

[0303] Comparison of the deduced BnSCL1 amino acid sequence to the NCBI (see URL:<http://www.ncbi.nlm.nih.gov>) and TAIR (see URL:[arabidopsis.org](http://arabidopsis.org)) databases results in a list of proteins with considerable similarity (FIG. 21). According to the NTI computer program

(InforMax, Inc.), BnSCL1 shares an 89% amino acid identity with AtSCL15 (Pysh et al., 1999) or VHS5 (Silverstone et al., 1998), an Arabidopsis SCARECROW-like protein (accession number Z99708, At4g36710), while it is 37% identical to AtSCR (accession number U62797). Interestingly, it also shares high similarity (66% sequence identity) with a tomato (*Lycopersicon esculentum*) protein (accession number AF273333), a member of the GRAS/VHIID protein family, encoded by the Lateral suppressor gene (Ls) (Schumacher et al., 1999) (FIG. 20). Consistent with these data, phylogenetic analysis using either NTI Vector or DNA Star program classified BnSCL1, AtSCL15 and LsSCL (Ls) in the same subgroup (FIG. 21).